

SEQUENCE LISTING

<110> ASAHIKASEI KOGYO KABUSHIKI KAISHA
 ASAHI MEDICAL CO., LTD.

<120> Separating apparatus of cells and separating method

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 JP 10/163023

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 Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly
 35 40 45
 AGT GCT TAC TAC AAT GAG ATG TTC AAG GGC AAG GCC ACA CTG ACT GCA 192
 Ser Ala Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala
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 Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 65 70 75 80
 GAG GAC TCT GCG GTC TAT TTC TGT GCA AGA CGC GGA ACT GGG ACG GGG 288
 Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly
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 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr
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 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
 65 70 75 80
 ACC TAT TAC TGT CAG CAA AGT AGT GAG GAT CCT CCG ACG TTC GGT GGA 288
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 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
 35 40 45
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Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
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TTC ACC CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT	336
Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr	
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Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr	
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Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly	
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GGT GGC GGA TCG CAG GTT CAG CTG CAG CAG TCT GGA CCT GAG CTG GTG	480
Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val	
145 150 155 160	
AAG CCT GGG GCT TCA GTG AAG ATG TCC TGC AAG GCT TCT GGA TAC ACA	528
Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr	
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TTC ACT GAC TAT GTT ATA AAC TGG TTG AAC CAG AGA ACT GGA CAG GGC	576
Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly	
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CTT GAG TGG ATT GGA GAG ATT TAT CCT GGA AGT GGT AGT GCT TAC TAC	624
Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr	
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AAC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG	720
Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala	
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GTC TAT TTC TGT GCA AGA CGC GGA ACT GGG ACG GGG TTT GCT TAC TGG	768
Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp	
245 250 255	
GGC CGA GGG ACT CTG GTC ACT GTC TCT GCA GCG GCC GCA GAC TAC AAG	816
Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Asp Tyr Lys	
260 265 270	
GAT GAC GAT GAC AAA GGC TCG AGC GAG CAG AAG CTG ATC AGC GAA GAG	864
Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu	
275 280 285	
GAT CTG GGC TCG AGG TCG ACC CAC CAT CAT CAT CAC CAC GGG TCG ACC	912
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Lys	
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GCC	CAG	CCG	GCC	ATG	GCC	CAG	GTT	CAG	CTG	CAG	CAG	TCT	GGA	CCT	GAG	96
Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	
			20					25					30			
CTG	GTG	AAG	CCT	GGG	GCT	TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGA	144
Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	
		35					40					45				
TAC	ACA	TTC	ACT	GAC	TAT	GTT	ATA	AAC	TGG	TTG	AAC	CAG	AGA	ACT	GGA	192
Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Ile	Asn	Trp	Leu	Asn	Gln	Arg	Thr	Gly	
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CAG	GGC	CTT	GAG	TGG	ATT	GGA	GAG	ATT	TAT	CCT	GGA	AGT	GGT	AGT	GCT	240
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	Tyr	Pro	Gly	Ser	Gly	Ser	Ala	
65					70					75					80	
TAC	TAC	AAT	GAG	ATG	TTC	AAG	GGC	AAG	GCC	ACA	CTG	ACT	GCA	GAC	AAA	288
Tyr	Tyr	Asn	Glu	Met	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
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TCC	TCC	AAC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	336
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TCT	GCG	GTC	TAT	TTC	TGT	GCA	AGA	CGC	GGA	ACT	GGG	ACG	GGG	TTT	GCT	384
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Gly	Thr	Gly	Thr	Gly	Phe	Ala	
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TAC	TGG	GGC	CGA	GGG	ACT	CTG	GTC	ACT	GTC	TCT	GCA	GGT	GGA	GGC	GGT	432
Tyr	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	
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Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	
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GAT	GCT	GCA	ACC	TAT	TAC	TGT	CAG	CAA	AGT	AGT	GAG	GAT	CCT	CCG	ACG	768

Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Glu	Asp	Pro	Pro	Thr		
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TTC	GGT	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA	GCG	GCC	GCA	GAC	TAC	AAG	816	
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GAT	GAC	GAT	GAC	AAA	GGC	TCG	AGC	GAG	CAG	AAG	CTG	ATC	AGC	GAA	GAG	864	
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GAT	CTG	GGC	TCG	AGG	TCG	ACC	CAC	CAT	CAT	CAT	CAC	CAC	GGG	TCG	ACC	912	
Asp	Leu	Gly	Ser	Arg	Ser	Thr	His	His	His	His	His	His	Gly	Ser	Thr		
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 35 40 45
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
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 35 40 45
 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser
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1				5					10					15			
TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGA	TAC	ACA	TTC	ACT	GAC	TAT		96
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr		
			20					25						30			
GTT	ATA	AAC	TGG	TTG	AAC	CAG	AGA	ACT	GGA	CAG	GGC	CTT	GAG	TGG	ATT		144
Val	Ile	Asn	Trp	Leu	Asn	Gln	Arg	Thr	Gly	Gln	Gly	Leu	Glu	Trp	Ile		
		35					40					45					
GGA	GAG	ATT	TAT	CCT	GGA	AGT	GGT	AGT	GCT	TAC	TAC	AAT	GAG	ATG	TTC		192
Gly	Glu	Ile	Tyr	Pro	Gly	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Glu	Met	Phe		
		50				55					60						
AAG	GGC	AAG	GCC	ACA	CTG	ACT	GCA	GAC	AAA	TCC	TCC	AAC	ACA	GCC	TAC		240
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Asn	Thr	Ala	Tyr		
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ATG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC	TAT	TTC	TGT		288
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys		
				85					90					95			
GCA	AGA	CGC	GGA	ACT	GGG	ACG	GGG	TTT	GCT	TAC	TGG	GGC	CGA	GGG	ACT		336
Ala	Arg	Arg	Gly	Thr	Gly	Thr	Gly	Phe	Ala	Tyr	Trp	Gly	Arg	Gly	Thr		
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CTG	GTC	ACT	GTC	TCT	GCA												354
Leu	Val	Thr	Val	Ser	Ala												
			115														

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Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp		
			20					25					30				
GGT	GAT	AGT	TAT	ATG	AAC	TGG	TAC	CAA	CAG	AAA	CCA	GGA	CAG	CCA	CCC		144

Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	
		35					40					45				
AAA	CTC	CTC	ATC	TAT	GCT	GCA	TCC	AAT	CTA	GAA	TCT	GGG	ATC	CCA	GCC	192
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	
	50					55					60					
AGG	TTT	AGT	GGC	AGT	GGG	TCT	GGG	ACA	GAC	TTC	ACC	CTC	AAC	ATC	CAT	240
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	
65					70					75					80	
CCT	GTG	GAG	GAG	GAG	GAT	GCT	GCA	ACC	TAT	TAC	TGT	CAG	CAA	AGT	AGT	288
Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	
				85					90					95		
GAG	GAT	CCT	CCG	ACG	TTC	GGT	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA		333
Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
			100					105					110			
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CAG	GTG	CAG	CTG	AAG	CAG	TCA	GGA	CCT	GGC	CTA	GTG	CAG	CCC	TCA	CAG	48
Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	Pro	Ser	Gln	
			5						10					15		
AGC	CTG	TCC	TTC	ATC	TGC	ACA	GTC	TCT	GGT	TTC	TCA	TTA	ACT	AGT	CAT	96
Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Ser	His	
			20					25					30			
GGT	GTA	CAC	TGG	GTT	CGC	CAG	TCT	CCA	GGA	AAG	GGT	CTG	GAG	TGG	CTG	144
Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	
		35				40						45				
GGA	GTG	ATA	TGG	GGT	GCT	GGA	AGG	ACA	GAC	TAT	AAT	GCA	GCT	TTC	ATA	192
Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Ile	
	50					55					60					
TCC	AGA	CTG	AGC	ATC	AGC	AGG	GAC	ATT	TCC	AAG	AGC	CAA	GTT	TTC	TTT	240
Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	Ser	Lys	Ser	Gln	Val	Phe	Phe	
65					70					75					80	
AAG	ATG	AAC	AGT	CTG	CAA	GTT	GAT	GAC	ACA	GCC	ATA	TAT	TAC	TGT	GCC	288
Lys	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	
			85					90						95		
AGA	AAT	AGG	TAC	GAG	AGC	TAC	TTT	GAC	TAC	TGG	GGC	CAA	GGC	ACC	ACT	336
Arg	Asn	Arg	Tyr	Glu	Ser	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
			100					105					110			
TCC	CTC	ACA	GTC	TCCü												351
Leu	Thr	Val	Ser	Ser												

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 Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
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 GAT CAG GCC TCC ATC TCT TGC AGA TCT AGT CAG AAC CTT GTA CAC AGT 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
 20 25 30
 AAT GGA AAT ACC TAT TTA CAT TGG TAC CTG CAG AAG CCA GGC CAG TCT 144
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 CCA AAT CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT GGG GTC CCA 192
 Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA GAA TTC ACA CTC AAG ATC 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile
 65 70 75 80
 AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TTC TGC TCT CAA AGT 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 ACA CAT GTT CCG CTC ACG TTC GGT GCT GGG ACC AAG GTG GAG CTG AAA 336
 Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys
 100 105 110
 CGG 339
 Arg

<210> 41
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<400> 41
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 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
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 AAC GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTT GTT CCT TTC TAT 96
 Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
 20 25 30
 GCG GCC CAG CCG GCC ATG GCC CAG GTG AAG CTG CAG CAG TCT GGA CCT 144
 Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
 35 40 45
 GGC CTA GTG CAG CCC TCA CAG AGC CTG TCC TTC ATC TGC ACA GTC TCT 192
 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
 50 55 60
 GGT TTC TCA TTA ACT AGT CAT GGT GTA CAC TGG GTT CGC CAG TCT CCA 240
 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
 65 70 75 80
 GGA AAG GGT CTG GAG TGG CTG GGA GTG ATA TGG GGT GCT GGA AGG ACA 288
 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
 85 90 95

GAC	TAT	AAT	GCA	GCT	TTC	ATA	TCC	AGA	CTG	AGC	ATC	AGC	AGG	GAC	ATT	336
Asp	Tyr	Asn	Ala	Ala	Phe	Ile	Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	
			100					105					110			
TCC	AAG	AGC	CAA	GTT	TTC	TTT	AAG	ATG	AAC	AGT	CTG	CAA	GTT	GAT	GAC	384
Ser	Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp	
			115					120					125			
ACA	GCC	ATA	TAT	TAC	TGT	GCC	AGA	AAT	AGG	TAC	GAG	AGC	TAC	TTT	GAC	432
Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Tyr	Glu	Ser	Tyr	Phe	Asp	
	130						135					140				
TAC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	480
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
145					150					155					160	
TCA	GGC	GGA	GGT	GGC	TCT	GGC	GGT	GGC	GGA	TCG	GAC	ATC	GAG	CTC	ACT	528
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	
				165					170					175		
CAG	TCT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT	GGA	GAT	CAG	GCC	TCC	ATC	576
Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
			180					185					190			
TCT	TGC	AGA	TCT	AGT	CAG	AAC	CTT	GTA	CAC	AGT	AAT	GGA	AAT	ACC	TAT	624
Ser	Cys	Arg	Ser	Ser	Gln	Asn	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
			195				200					205				
TTA	CAT	TGG	TAC	CTG	CAG	AAG	CCA	GGC	CAG	TCT	CCA	AAT	CTC	CTG	ATC	672
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Asn	Leu	Leu	Ile	
	210					215					220					
TAC	AAA	GTT	TCC	AAC	CGA	TTT	TCT	GGG	GTC	CCA	GAC	AGG	TTC	AGT	GGC	720
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
225					230					235					240	
AGT	GGA	TCA	GGG	ACA	GAA	TTC	ACA	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	768
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	
				245					250					255		
GAG	GAT	CTG	GGA	GTT	TAT	TTC	TGC	TCT	CAA	AGT	ACA	CAT	GTT	CCG	CTC	816
Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	
			260					265					270			
ACG	TTC	GGT	GCT	GGG	ACC	AAG	GTG	GAG	CTG	AAA	CGG	GCG	GCC	GCA	GGT	864
Thr	Phe	Gly	Ala	Gly	Thr	Lys	Val	Glu	Leu	Lys	Arg	Ala	Ala	Ala	Gly	
		275					280					285				
GCG	CCG	GTG	CCG	TAT	CCG	GAT	CCG	CTG	GAA	CCG	CGT	GCC	GCA	TAG		909
Ala	Pro	Val	Pro	Tyr	Pro	Asp	Pro	Leu	Glu	Pro	Arg	Ala	Ala			
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 <212> DNA
 <213> mouse

<400> 42
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 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
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AAC	GTG	AAA	AAA	TTA	TTA	TTC	GCA	ATT	CCT	TTA	GTT	GTT	CCT	TTC	TAT	96
Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	Phe	Tyr	
		20						25					30			
GCG	GCC	CAG	CCG	GCC	ATG	GCC	CAG	GTG	AAG	CTG	CAG	CAG	TCT	GGA	CCT	144
Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Pro	
		35					40					45				
GGC	CTA	GTG	CAG	CCC	TCA	CAG	AGC	CTG	TCC	TTC	ATC	TGC	ACA	GTC	TCT	192
Gly	Leu	Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	
	50					55				60						
GGT	TTC	TCA	TTA	ACT	AGT	CAT	GGT	GTA	CAC	TGG	GTT	CGC	CAG	TCT	CCA	240
Gly	Phe	Ser	Leu	Thr	Ser	His	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	
	65				70				75					80		
GGA	AAG	GGT	CTG	GAG	TGG	CTG	GGA	GTG	ATA	TGG	GGT	GCT	GGA	AGG	ACA	288
Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	
			85					90					95			
GAC	TAT	AAT	GCA	GCT	TTC	ATA	TCC	AGA	CTG	AGC	ATC	AGC	AGG	GAC	ATT	336
Asp	Tyr	Asn	Ala	Ala	Phe	Ile	Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	
		100						105					110			
TCC	AAG	AGC	CAA	GTT	TTC	TTT	AAG	ATG	AAC	AGT	CTG	CAA	GTT	GAT	GAC	384
Ser	Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp	
		115					120					125				
ACA	GCC	ATA	TAT	TAC	TGT	GCC	AGA	AAT	AGG	TAC	GAG	AGC	TAC	TTT	GAC	432
Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Tyr	Glu	Ser	Tyr	Phe	Asp	
	130					135					140					
TAC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGA	GGC	GGT	480
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
	145				150					155					160	
TCA	GGC	GGA	GGT	GGC	TCT	GGC	GGT	GGC	GGA	TCG	GAC	ATC	GAG	CTC	ACT	528
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	
			165					170					175			
CAG	TCT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT	GGA	GAT	CAG	GCC	TCC	ATC	576
Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
		180						185					190			
TCT	TGC	AGA	TCT	AGT	CAG	AAC	CTT	GTA	CAC	AGT	AAT	GGA	AAT	ACC	TAT	624
Ser	Cys	Arg	Ser	Ser	Gln	Asn	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
		195					200					205				
TTA	CAT	TGG	TAC	CTG	CAG	AAG	CCA	GGC	CAG	TCT	CCA	AAT	CTC	CTG	ATC	672
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Asn	Leu	Leu	Ile	
	210					215					220					
TAC	AAA	GTT	TCC	AAC	CGA	TTT	TCT	GGG	GTC	CCA	GAC	AGG	TTC	AGT	GGC	720
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
	225				230					235					240	
AGT	GGA	TCA	GGG	ACA	GAA	TTC	ACA	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	768
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	
			245						250					255		
GAG	GAT	CTG	GGA	GTT	TAT	TTC	TGC	TCT	CAA	AGT	ACA	CAT	GTT	CCG	CTC	816
Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	
		260					265						270			
ACG	TTC	GGT	GCT	GGG	ACC	AAG	GTG	GAG	CTG	AAA	CGG	GCG	GCC	GCA	GGT	864

Thr	Phe	Gly	Ala	Gly	Thr	Lys	Val	Glu	Leu	Lys	Arg	Ala	Ala	Ala	Gly	
						275					280				285	
GCG	CCG	GTG	CCG	TAT	CCG	GAT	CCG	CTG	GAA	CCG	CGT	GCC	GCA	AAG		909
Ala	Pro	Val	Pro	Tyr	Pro	Asp	Pro	Leu	Glu	Pro	Arg	Ala	Ala	Lys		
	290					295					300					
AAG	AAG	TAG														918
Lys	Lys															
	305															

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 <223> Amino acid sequence of heavy chain CDR-1

<400> 43
 Ser His Gly Val His

<210> 44
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 <212> PRT
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 Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile Ser
 1 5 10 15

<210> 45
 <211> 9
 <212> PRT
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<400> 45
 Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr

<210> 46
 <211> 16
 <212> PRT
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<400> 46
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Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe

<210> 48
<211> 9
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<400> 48
Ser Gln Ser Thr His Val Pro Leu Thr